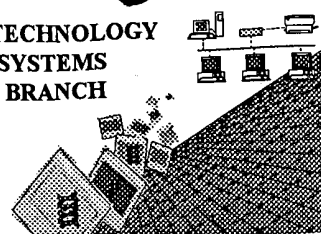


650-622-2499

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



#15  
pg 5/8/02

## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/59,466B 11634  
Source: 1600  
Date Processed by STIC: 4/29/2002

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.  
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**  
**VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name,  
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,  
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,  
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER:

09/59,466B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 \_\_\_\_\_ Wrapped Nucleics  
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 \_\_\_\_\_ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 \_\_\_\_\_ Misaligned Amino  
Numbering

The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 \_\_\_\_\_ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 \_\_\_\_\_ Variable Length

Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 \_\_\_\_\_ PatentIn 2.0  
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 \_\_\_\_\_ Skipped Sequences  
(OLD RULES)

Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 \_\_\_\_\_ Skipped Sequences  
(NEW RULES)

Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000

9 \_\_\_\_\_ Use of n's or Xaa's  
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 \_\_\_\_\_ Invalid <213>  
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 \_\_\_\_\_ Use of <220>

Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 \_\_\_\_\_ PatentIn 2.0  
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 \_\_\_\_\_ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

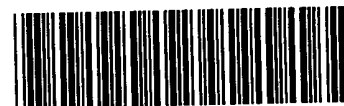
AMC/MH - Biotechnology Systems Branch - 08/21/2001

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FYI



1600

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/591,466B

DATE: 04/29/2002  
TIME: 16:40:33

*pg 1-3*

Input Set : A:\032266-003.ST25.txt  
Output Set: N:\CRF3\04292002\I591466B.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: Von Schaewen, Antje  
5 <120> TITLE OF INVENTION: Plant GntI Sequences and the Use Thereof for the Production  
6 of Plants Having Reduced or Lacking N-acetyl Glucosaminyl  
7 Transferase I(GnTI) Activity  
9 <130> FILE REFERENCE: 032266-003  
11 <140> CURRENT APPLICATION NUMBER: US 09/591,466B  
12 <141> CURRENT FILING DATE: 2000-06-09  
14 <150> PRIOR APPLICATION NUMBER: EP 98/08001  
15 <151> PRIOR FILING DATE: 1998-09-12  
17 <160> NUMBER OF SEQ ID NOS: 14  
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0

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# ERRORED SEQUENCES

447 <210> SEQ ID NO: 4  
448 <211> LENGTH: 446  
449 <212> TYPE: PRT  
450 <213> ORGANISM: Nicotiana tabacum  
E--> 452 <400> SEQUENCE: *46 insert 4*  
453 Met Arg Gly Asn Lys Phe Cys Cys Asp Phe Arg Tyr Leu Leu Ile Leu  
454 1 5 10 15  
455 Ala Ala Val Ala Phe Ile Tyr Thr Gln Met Arg Leu Phe Ala Thr Gln  
456 20 25 30  
457 Ser Glu Tyr Ala Asp Arg Leu Ala Ala Ile Glu Ala Glu Asn His  
458 35 40 45  
459 Cys Thr Ser Gln Thr Arg Leu Ile Asp Gln Ile Ser Leu Gln Gln  
460 50 55 60  
461 Gly Arg Ile Val Ala Leu Glu Glu Met Lys Arg Gln Asp Gln Glu  
462 65 70 75 80  
463 Cys Arg Gln Leu Arg Ala Leu Val Gln Asp Leu Glu Ser Lys Gly Ile  
464 85 90 95  
465 Lys Lys Leu Ile Gly Asn Val Gln Met Pro Val Ala Ala Val Val Val  
466 100 105 110  
467 Met Ala Cys Asn Arg Ala Asp Tyr Leu Glu Lys Thr Ile Lys Ser Ile  
468 115 120 125  
469 Leu Lys Tyr Gln Ile Ser Val Ala Ser Lys Tyr Pro Leu Phe Ile Ser  
470 130 135 140  
471 Gln Asp Gly Ser His Pro Asp Val Arg Lys Leu Ala Leu Ser Tyr Asp  
472 145 150 155 160  
473 Gln Leu Thr Tyr Met Gln His Leu Asp Phe Glu Pro Val His Thr Glu  
474 165 170 175  
475 Arg Pro Gly Glu Leu Ile Ala Tyr Tyr Lys Ile Ala Arg His Tyr Lys

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*(only the errored portion of  
Sequence 4  
is shown)*

<210> 1  
 <211> 1669  
 <212> DNA  
 <213> Solanum tuberosum

<220>  
 <221> misc\_feature  
 <222> (659)...(667)  
 <223> function: Asn codon in this context is a potential  
 glycosylation site;  
 product: N-glycosylation consensus sequence;  
 phenotype: N-glycans modulate protein properties;  
 standard\_name: N-glycosylation site;  
 label: pot-CHO;  
 note: GnTI-coding sequences from animals do not  
 contain this feature.

global err

insert  
 <220>

misspelled - replace  
 with "glycosylation"

Per 1.823 of Sequence Rules, each  
 <223> section has a maximum of 4 lines.

Please insert a <220> after each group of  
4 lines.

IMPORTANT

The types of errors shown exist throughout  
 the Sequence Listing. Please check subsequent  
 sequences for similar errors.

09/09/1,466B 3

<210> 6  
<211> 444  
<212> PRT  
<213> ←  
<400> 6

insert this mandatory numeric identifier and its response

(see item 10 on Error Summary Sheet)

PJ I

Use of n and/or Xaa has been detected in the Sequence Listing.  
Review the Sequence Listing to insure a corresponding  
explanation is presented in the <220> to <223> fields of  
each sequence using n or Xaa.